



PATENT
Our Docket: P-IS 4367

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of:)	Examiner: M. Davis
Biaoyang Lin)	
Serial No.: 09/729,653)	Group Art Unit: 1642
Filed: December 4, 2000)	
For: PROSTATE-SPECIFIC POLYPEPTIDE)	
PAMP AND ENCODING NUCLEIC)	
ACID MOLECULES)	

ASST COMMISSIONER OF PATENTS
WASHINGTON, D.C. 20231

Sir:

DECLARATION UNDER 37 C.F.R. § 1.131

I, the undersigned, hereby declare as follows:

1. I am the Biaoyang Lin who is named as the sole inventor of the above-identified application.
2. I performed or supervised the experiments that resulted in obtaining PAMP nucleic acid sequence corresponding to residues 864 to 1382 of SEQ ID NO: 2 prior to September 8, 2000, which is the date I have been informed that the Nagase et al. KIAA1638 sequence identified by ID Q9HCD4 was first made available to the public. The Genbank accession number for sequence ID Q9HCD4 is AB046858, as shown in Exhibit 1. The relevant statement from a representative of the DNA Data Bank of Japan (DDBJ) attesting that this sequence was released to the public on September 8, 2000, is attached hereto as Exhibit 2.
3. The work leading to obtaining PAMP nucleic acid sequence corresponding to residues 864 to 1382 of SEQ ID NO: 2 was

Inventor Biaoyang Lin
Serial No.: 09/729,653
Filed: December 4, 2000
Page 2

performed by me or under my supervision prior to
September 8, 2000.

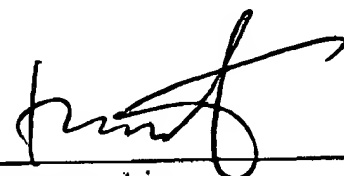
4. As evidence that I had obtained and sequenced one or more nucleic acid molecules encoding residues 864 to 1382 of the human PAMP sequence shown in the above-identified patent application as SEQ ID NO: 2, I have attached photocopies of laboratory records, the dates of which have been redacted but which are prior to September 8, 2000. Specifically, Exhibit 3 attached hereto is the nucleic acid sequence and translated sequence of a GST-PAMP fusion protein including residues 864 to 1382 of SEQ ID NO: 2.
5. The sequence shown in Exhibit 3 represents the nucleic acid sequence and amino acid sequence corresponding to a GST-PAMP fusion protein that includes residues 864 to 1382 of PAMP. In particular, the translated sequence beginning at approximately nucleotide 675 of Exhibit 3, "MGDIRR," represents the PAMP amino acid sequence beginning at residue 864 of SEQ ID NO: 2, and the translated sequence beginning at approximately nucleotide 2215 of Exhibit 3, "RTEEEL," represents amino acids 1377 to 1382 of PAMP SEQ ID NO: 2. Although the "last modified" date of the computer file shown as Exhibit 3 has been redacted, the date is prior to September 8, 2000.
6. The results discussed in paragraphs 3 to 5 above demonstrate that I had obtained PAMP nucleic acid sequence corresponding to the amino acid sequence of residues 864 to 1382 of SEQ ID NO: 2 prior to September 8, 2000.

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7. I do not know and do not believe that the invention was in the public prior to the time I conceived of the invention and reduced it to practice and I have never abandoned the application.

I declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that willful false statements may jeopardize the validity of the application or any patent issuing thereon.

Oct 31, 2002
Date


Biaoyang Lin

GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Kun On: May 21, 2002, 14:49:40 ; Search time 50.02 Seconds
(without alignments)
4779.668 Million cell updates/sec

Title: US-09-729-653-2
Perfect score: 7257

Sequence: 1 NSLGRCSKGLGCHAVAC.....AAQLKISDCTQYLRTEEL 1302
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_19:..
1: sp_archaea:..
2: sp_bacteria:..
3: sp_fungi:..
4: sp_human:..
5: sp_invertebrate:..
6: sp_mammal:..
7: sp_mhc:..
8: sp_organelle:..
9: sp_phage:..
10: sp_plant:..
11: sp_rodent:..
12: sp_virus:..
13: sp_unclassified:..
14: sp_virus:..
15: sp_virus:..
16: sp_bacteriaph:..
17: sp_archaeap:..

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4700	64.8	905	4 Q9HCD4	Q9hcd4 homo sapien
2	2780	38.3	1366	5 Q9V8W2	Q9v8w2 drosophila
3	2354	32.4	481	4 Q9H5S0	Q9h5s0 homo sapien
4	1157	15.9	519	5 Q46018	Q46018 caenorhabdi
5	924	12.7	634	5 Q46020	Q46020 caenorhabdi
6	289	4.0	1205	5 Q9W097	Q9w097 drosophila
7	289	4.0	1749	11 Q9JKU3	Q9jku3 rattus norv
8	271.5	3.7	1242	4 Q9H8C6	Q9h8c6 homo sapien
9	270.5	3.7	1758	5 Q22830	Q22830 caenorhabdi
10	268.5	3.7	1292	4 Q9H8C5	Q9h8c5 homo sapien
11	263	3.6	1198	4 Q9UF80	Q9uf80 homo sapien
12	263	3.6	1241	4 Q9HAT9	Q9hat9 homo sapien
13	256.5	3.5	1462	4 Q60332	Q60332 homo sapien
14	251.5	3.5	1653	4 Q90C01	Q9u0c1 homo sapien
15	248.5	3.4	1462	4 Q96RY7	Q96ry7 homo sapien
16	246	3.4	1131	4 Q9BTB9	Q9bcb9 homo sapien

17	246	3.4	1160	4	Q9BTY4	Q9bty4 homo sapien
18	235.5	3.2	993	4	Q9RV68	Q9rv68 homo sapien
19	235	3.2	1443	5	Q9VPR0	Q9vpr0 drosophila
20	223.5	3.1	955	4	Q9H7P3	Q9h7p3 homo sapien
21	218	3.0	764	4	Q9P2H3	Q9p2h3 homo sapien
22	216.5	3.0	864	4	Q9H9Z0	Q9h9z0 homo sapien
23	215.5	3.0	705	4	Q96KK0	Q96kk0 homo sapien
24	209.5	2.9	1307	5	P90757	P90757 caenorhabdi
25	206	2.8	821	4	Q9NUW6	Q9nuw6 homo sapien
26	190.5	2.6	1119	5	O18B59	O18b59 caenorhabdi
27	190	2.6	766	4	Q9P2L0	Q9p2l0 homo sapien
28	185	2.5	1090	4	Q9ULP1	Q9ulp1 homo sapien
29	183.5	2.5	588	4	Q96KK1	Q96kk1 homo sapien
30	183.5	2.5	656	4	Q9UG52	Q9ug52 homo sapien
31	180	2.5	601	11	Q91YV4	Q91yv4 mus musculu
32	178	2.5	1047	5	O45401	O45401 caenorhabdi
33	174.5	2.4	968	5	O9VSJ6	O9vsj6 drosophila
34	171.5	2.4	1319	10	Q9FNA4	Q9fna4 arabidopsis
35	170	2.3	887	5	Q9H040	Q9h040 drosophila
36	164	2.3	472	10	Q9PFTB	Q9pftb arabidopsis
37	164	2.3	493	4	Q9U196	Q9u196 homo sapien
38	164	2.3	493	4	O75869	O75869 homo sapien
39	164	2.3	504	4	Q9ULH8	Q9ulh8 homo sapien
40	163	2.2	496	4	Q9UM11	Q9um11 homo sapien
41	161.5	2.2	558	4	Q9DFJ9	Q9dfj9 homo sapien
42	161.5	2.2	911	10	Q9LW07	Q9lw07 arabidopsis
43	161.5	2.2	1223	4	Q9UF15	Q9uf15 homo sapien
44	161	2.2	493	11	Q9RIK5	Q9rik5 mus musculu
45	161	2.2	493	13	O42585	O42585 xenopus lae

ALIGNMENTS

RESULT	1
Q9HCD4	
ID	Q9HCD4
AC	Q9HCD4; PRELIMINARY; PRT; 905 AA.
DT	01-MAR-2001 (TREMBLrel. 16, Created)
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE	KIAA1638 PROTEIN (FRAGMENT).
GN	KIAA1638
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OX	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE-20450683; PubMed-10997877;
RA	Nagase T., Kikuno K., Nakayama M., Hirose M., Ohara O.;
RT	*Prediction of the coding sequences of unidentified human genes.
RT	XVIII. The complete sequences of 100 new cDNA clones from brain which
RL	code for large proteins in vitro.*;
RL	DNA Res. 7:273-281(2000).
DR	EMBL; AB046858; BAB13464.1;
DR	InterPro; IPR000547; Clathrin_repeat.
DR	SMART; SM00299; CLU; 1.
FT	NON_TER 1
SQ	SEQUENCE 905 AA; 102450 MW; FP370996F00FE1BF CRC64;
Query Match	64.8%; Score 4700; DB 4; Length 905;
Best Local Similarity	99.8%; Pred. No. 0;
Matches	903; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	375 ALSTQSGSLVFLTKLPTLGDACSTRIAYLTSLLEVTVANPVEGELPTVSDVDPHYA 434
DB	1 ALSTQSGSLVFLTKLPTLGDACSTRIAYLTSLLEVTVANPVEGELPTVSDVDPHYA 60
QY	435 VGLYHLAVCHNRHRAFYVLGENAVKKLDMKEYLGTVAISCLISDYAAALFECKVOLHIE 494
DB	61 VGLYHLAVCHNRHRAFYVLGENAVKKLDMKEYLGTVAISCLISDYAAALFECKVOLHIE 120

From: <ddbjupdt@ddbj.nig.ac.jp>
To: <KLemme@candf.com>
Date: 8/25/02 7:14PM
Subject: Re: ABO46858

Dear Dr. Kristen Lemme

The sequence data with accession number ABO46858 were released from the DNA Data Bank of Japan (DDBJ) on Sep. 8 2000 in order to make them public.

DDBJ is in collaboration with the EMBL Nucleotide Sequence Database in Europe and GenBank in USA to form and function as the International Nucleotide Sequence Databases.

We take no responsibility for the priority and property issues for the submitted data. We simply inform you of the releasing date on request.

We appreciate your understanding and cooperation.

Sincerely yours,

Yoshio Tateho, Ph.D.
DNA Data Bank of Japan
National Institute of Genetics

>Date: Wed, 21 Aug 2002 14:09:57 -0400 (EDT)
>Subject: ATTN-Info-DR-ABO46858
>To: ddbjupdt@ddbj.nig.ac.jp

>Dear DDBJ,

>

>I am forwarding a release date request for a patent inquiry.

>Please reply directly to the user. Thank you for your help.

>

>Regards,

>Monica L. Romiti

>GenBank User Services

>

>----- Begin Forwarded Message -----

>

>Date: Tue, 20 Aug 2002 10:53:30 -0700

>From: "Kristen Lemme" <KLemme@candf.com>

>To: <gb-admin@ncbi.nlm.nih.gov>

>Subject: ABO46858

>Dear Sirs:

>

>We would like to know the first date that GenBank Accession Number

>ABO46858 was available to the public through GenBank.

>

>Sincerely,

>

>Kristen Lemme

>Assistant to Andrea L. Gashler, Ph.D.

>

>Ms. Kristen Lemme

>CAMPBELL & FLORES LLP

>4370 La Jolla Village Drive

>7th Floor

>San Diego, California 92122

>

>Telephone: (858) 535-9001

>Facsimile: (858) 597-1585

>

>=====

>The information contained in this e-mail is confidential, may be
>attorney-client privileged, and is intended for the use of the
>individual or entity named above. If you have received this
>e-mail in error, please contact the sender. Thank you.

>

>Date: Wed, 21 Aug 2002 11:33:33 -0700

>From: "Kristen Lemme" <KLemme@candf.com>

>To: <ddbjupdt@ddbj.nig.ac.jp>

>Subject: ABO46858

>Dear Sirs:

>

>We would like to know the first date that GenBank Accession Number
>ABO46858 was available to the public through GenBank.

>

>Sincerely,

>

>Kristen Lemme

>Assistant to Andrea L. Gashler, Ph.D.

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>Ms. Kristen Lemme

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>San Diego, California 92122

>

>Telephone: (858) 535-9001

>Facsimile: (858) 597-1585

>

>=====

>The information contained in this e-mail is confidential, may be
>attorney-client privileged, and is intended for the use of the
>individual or entity named above. If you have received this
>e-mail in error, please contact the sender. Thank you.

>Date: Wed, 21 Aug 2002 16:08:20 -0700

>From: "Kristen Lemme" <KLemme@candf.com>

>To: <ddbjupdt@ddbj.nig.ac.jp>

>Subject: ABO46858

>Dear Sirs:

>

>We would like to know the first date that GenBank Accession Number

>ABO46858 was available to the public through GenBank.

>

>Sincerely,

>

>Kristen Lemme

>Assistant to Andrea L. Gashler, Ph.D.

>

--

CC: <ytateno@genes.nig.ac.jp>, <hsugawar@genes.nig.ac.jp>, <ddbjupdt@ddbj.nig.ac.jp>

9E1_pEGFPconstruct Translated Sequence

```

      10      20      30      40      50
TAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATA
ATCAATAATTATCATTAGTTAATGCCCCAGTAATCAAGTATCGGGTATAT
*  L  L  I  V  I  N  Y  G  V  I  S  S  *  P  I  Y>
_____TRANSLATION OF 9E1_PEGFPCONSTRUCT (A)_____>

      60      70      80      90     100
TGGAGTTCGCGGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACCG
ACCTCAAGGCGCAATGTATTGAATGCCATTTACCGGGCGGACCGACTGGC
  G  V  P  R  Y  I  T  Y  G  K  W  P  A  W  L  T>
_____TRANSLATION OF 9E1_PEGFPCONSTRUCT (A)_____>

     110     120     130     140     150
CCCAACGACCCCCGCCCCATTGACGTCAATAATGACGTATGTTCCCATAGT
GGGTTGCTGGGGGCGGGTAACTGCAGTTATTACTGCATACAAGGGTATCA
A  Q  R  P  P  P  I  D  V  N  N  D  V  C  S  H  S>
_____TRANSLATION OF 9E1_PEGFPCONSTRUCT (A)_____>

     160     170     180     190     200
AACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGT
TTGCGGTTATCCCTGAAAGGTAAGTGCAGTTACCCACCTCATAAATGCCA
N  A  N  R  D  F  P  L  T  S  M  G  G  V  F  T  V>
_____TRANSLATION OF 9E1_PEGFPCONSTRUCT (A)_____>

     210     220     230     240     250
AAACTGCCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCC
TTTGACGGGTGAACCGTCATGTAGTTACATAGTATACGGTTTCATGCGGG
N  C  P  L  G  S  T  S  S  V  S  Y  A  K  Y  A>
_____TRANSLATION OF 9E1_PEGFPCONSTRUCT (A)_____>

     260     270     280     290     300
CCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTA
GGATACTGCAGTTACTGCCATTTACCGGGCGGACCGTAATACGGGTCAT
P  Y  *  R  Q  *  R  *  M  A  R  L  A  L  C  P  V>
_____TRANSLATION OF 9E1_PEGFPCONSTRUCT (A)_____>

     310     320     330     340     350
CATGACCTTATGGGACTTTCTTACTTGGCAGTACATCTACGTATTAGTCA
GTACTGGAATACCCTGAAAGGATGAACCGTCATGTAGA/GCATAATCAGT
H  D  L  M  G  L  S  Y  L  A  V  H  L  R  I  S  H>
_____TRANSLATION OF 9E1_PEGFPCONSTRUCT (A)_____>

     360     370     380     390     400
TCGCTATTACCATGGTGATGCGGTTTTTGGCAGTACATCAATGGGCGTGGA
AGCGATAATGGTACCACTACGCCAAAACCGTCATGTAGTTACCCGCACCT
R  Y  Y  H  G  D  A  V  L  A  V  H  Q  W  A  W>
_____TRANSLATION OF 9E1_PEGFPCONSTRUCT (A)_____>

     410     420     430     440     450
TAGCGGTTTTGACTCACGGGATTTCCAAGTCTCCACCCCATTGACGTCA
ATCGCCAAACTGAGTGCCCCCTAAAGGTTTCAGAGGTGGGGTAACTGCAGTT
I  A  V  *  L  T  G  I  S  K  S  P  P  H  *  R  Q>
_____TRANSLATION OF 9E1_PEGFPCONSTRUCT (A)_____>

     460     470     480     490     500
TGGGAGTTTGTTTTGGCACCAAPATCAACGGGACTTTCCAAAATGTCGTA

```


9E1_pEGFPconstruct Translated Sequence

ACCCCTCAAACAAACCCTGCTTTTAGTTGCCCTGAAAGGTTTTACAGCAT
W E F V L A P K S T G L S K M S *>
____TRANSLATION OF 9E1_PEGFPCONSTRUCT [A]____>

510 520 530 540 550
ACAACCTCCGCCCATTTGACGCAATGGGCGGTAGGCGTGTACGGTGGGAG
TGTTGAGGCGGGGTAACCTGCGTTTACCCGCCATCCGCACATGCCACCCTC
Q L R P I D A N G R * A C T V G>
____TRANSLATION OF 9E1_PEGFPCONSTRUCT [A]____>

560 570 580 590 600
GTCTATATPAGCAGAGCTGGTTTAGTGAACCGTCAGATCCGCTAGCGCTA
CAGATATATTCTGTCGACCAATCACTTGGCAGTCTAGGCCATCGCGAT
G L Y K Q S W F S E P S D P L A L>
____TRANSLATION OF 9E1_PEGFPCONSTRUCT [A]____>

610 620 630 640 650
CCGGACTCAGATCTCGAGCTCAAGCTTCGAATTCGACGTCGACGGTACC
GGCCTGAGTCTAGAGCTCGAGTTCGAAGCTTAAGACGTCAGCTGCCATGG
P D S D L E L K L R I L Q S T V P>
____TRANSLATION OF 9E1_PEGFPCONSTRUCT [A]____>

660 670 680 690 700
GCGGGCCCGGGATCCGGCCACCATGGGAGACATACGTCGAGGGGTAAACC
CGCCCCGGGCCCTAGGCCGGTGGTACCCTCTGTATGCAGCTCCCCAATTGG
R A R D P A T M G D I R R G V N>
____TRANSLATION OF 9E1_PEGFPCONSTRUCT [A]____>

710 720 730 740 750
AAGCCCTCAAGCATCCCAGCAGGGTCCTTAAAAGAGACTGTGGAGCCATA
TTCGGGAGTTCGTAGGGTCGTCGAGGAATTTCTCTGACACCTCGGTAT
Q A L K H P S R V L K R D C G A I>
____TRANSLATION OF 9E1_PEGFPCONSTRUCT [A]____>

760 770 780 790 800
TTGGAGAATATGAACCAATTTTCAGAAGCGGCCCACTGTATGAAAPAGG
AACCTCTTATACTTCGTTAAAGTCTTCGCCGGGTGTACATACTTTTTC
L E N M K Q F S E A A Q L Y E K G>
____TRANSLATION OF 9E1_PEGFPCONSTRUCT [A]____>

810 820 830 840 850
TCTCTACTACGATAAAGCAGCATCTGTTTACATCCGCTCTAAGAAATTGGG
AGAGATGATGCTATTTTCGTCGTAGACAAATGTAGGCGAGATTCTTAACCC
L Y Y D K A A S V Y I R S K N W>
____TRANSLATION OF 9E1_PEGFPCONSTRUCT [A]____>

860 870 880 890 900
CAAAAGTTGGTGATCTTCTGCCCCACGTTTCTTCTCCTAAGATCCATTTG
GTTTTCAACCACTAGAAGACGGGGTGCAAAGAAGAGGATTCTAGGTAAC
A K V G D L L P H V S S P K I H L>
____TRANSLATION OF 9E1_PEGFPCONSTRUCT [A]____>

910 920 930 940 950
CAGTATGCCAAGCCAAGGAGCAGATGGAAGATACAAAGAACTGTTGT
GTCATACGGTTTCGGTTCCTTCGTCTACCTTCTATGTTTCTTCGACACCA
Q Y A K A K E A D G R Y K E A V V>
____TRANSLATION OF 9E1_PEGFPCONSTRUCT [A]____>

9E1_pEGFPconstruct Translated Sequence

```

      960      970      980      990     1000
AGCTTTATGAAAATGCAAAACAGTGGCAAAGTGTAAATCCGCATCTATCTGG
TCGAATACTTTTACGTTTTGTCAACCGTTTCACATTAGCGGTAGATAGACC
  A Y E N A K Q W Q S V I R I Y L>
_____TRANSLATION OF 9E1_PEGFPConstruct (A)_____>

      1010     1020     1030     1040     1050
ATCACCTCAATAATCCTGAAAAGCTGTCAATATTGTTAGAGAGACCCAG
TAGTGGAGTTATTAGGACTTTTTCGACAGTTATAACAATCTCTCTGGGTC
D H L N N P E K A V N I V R E T Q>
_____TRANSLATION OF 9E1_PEGFPConstruct (A)_____>

      1060     1070     1080     1090     1100
TCTCTGGATGGAGCCAAATGGTAGCCAGGTTTTTTCTACAGCTTGGTGA
AGAGACCTACCTCGGTTTTACCATCGGTCCAAAAAGATGTCTGAACCACT
S L D G A K M V A R F F L Q L G D>
_____TRANSLATION OF 9E1_PEGFPConstruct (A)_____>

      1110     1120     1130     1140     1150
CTATGGGTCTGCCATCCAGTTTCTTGTCATGTCCAAATGCAACAATGAAG
GATACCCAGACGGTAGGTCAAAGAACAGTACAGTTTACGTTGTTACTTC
Y G S A I Q F L V M S K C N N E>
_____TRANSLATION OF 9E1_PEGFPConstruct (A)_____>

      1160     1170     1180     1190     1200
CTTTCACACTGGCTCAGCAACACAACAAATGGAAATCTAKSMAGATATT
GAAAGTGTGACCGAGTCGTTGTGTGTTTACCTTTAGATMSKTCTATAA
A F T L A Q Q H N K M E I X X D I>
_____TRANSLATION OF 9E1_PEGFPConstruct (A)_____>

      1210     1220     1230     1240     1250
ATTGGTTCTGAAGACACTACTAATGAAGACTATCAAAGCATTGCCTTATA
TAACCAAGACTTCTGTGATGATTACTTCTGATAGTTTCGTAACGGAATAT
I G S E D T T N E D Y Q S I A L Y>
_____TRANSLATION OF 9E1_PEGFPConstruct (A)_____>

      1260     1270     1280     1290     1300
CTTTGAAGGARRAAAGAGATATCTTMAAGCGTGGAAAATTCTTCTTGCTGT
GAAACTTCCTYYTTCTCTATAGAAKTCCGACCTTTTAAGAAGAACGACA
F E G X K R Y L X A G K F F L L>
_____TRANSLATION OF 9E1_PEGFPConstruct (A)_____>

      1310     1320     1330     1340     1350
GTGGCCAATATTACAGGCACTTAVACACTTCCTGAAATGCCCAAGCTCG
CACCGGTTATAAGTGCTCGTGAATBTGTGAAGGACTTTACGGGTTGAGC
C G Q Y S R A L X H F L K C P S S>
_____TRANSLATION OF 9E1_PEGFPConstruct (A)_____>

      1360     1370     1380     1390     1400
GAAGATAATGTGGCAATAGAAATGGCAATTGAAACTGTTGGTCAGGCCAA
CTTCTATTACACCGTTATCTTTACCGTTAACTTTGACAAACAGTCCCGGTT
E D N V A I E M A I E T V G Q A K>
_____TRANSLATION OF 9E1_PEGFPConstruct (A)_____>

      1410     1420     1430     1440     1450
AGATGAAGTGTGACCAATCAGCTGATAGACCATCTCCTGGGGGAGAACG

```

9E1_pEGFPconstruct Translated Sequence

TCTACTTGACGACTGGTTAGTCGACTATCTGGTAGAGGACCCCTCTTGC
 D E L L T N Q L I D H L L G E N>
 _____TRANSLATION OF 9E1_PEGFPCONSTRUCT (A)_____>

1460 1470 1480 1490 1500
 ATGGCATGCCTAAGGATGCCAAGTACCTGTTCCGCTTGACATGGCTCTG
 TACCGTACGGATTCTTACGGTTCATGGACAAGGCGAATCATGTACCGAGAC
 D G M P K D A K Y L F R L Y M A L>
 _____TRANSLATION OF 9E1_PEGFPCONSTRUCT (A)_____>

1510 1520 1530 1540 1550
 AAGCAATACCGAGAAGCTGCCCAGACTGCCATCATCATTGCCAGAGAAGA
 TTCGTTATGGCTCTTCGACGGGTCTGACGGTAGTAGTAACGGTCTCTTCT
 K Q Y R E A A Q T A I I I A R E E>
 _____TRANSLATION OF 9E1_PEGFPCONSTRUCT (A)_____>

1560 1570 1580 1590 1600
 GCAGTCTGCAGGCAACTACCGGAATGCACACGATGTTCTCTTCAGTATGT
 CGTCAGACGTCCGTTGATGGCCTTACGTGTGCTACAAGAGAAGTCATACA
 Q S A G N Y R N A H D V L F S M>
 _____TRANSLATION OF 9E1_PEGFPCONSTRUCT (A)_____>

1610 1620 1630 1640 1650
 ATGCAGAACTGAAATCCCAGAAGATCAAAATTCCCTCCGAGATGGCCACC
 TACGTCTTGACTTTAGGGTCTTCTAGTTTTAAGGGAGGCTCTACCGGTGG
 Y A E L K S Q K I K I P S E M A T>
 _____TRANSLATION OF 9E1_PEGFPCONSTRUCT (A)_____>

1660 1670 1680 1690 1700
 AACCTCATGATTCTGCACAGCTATATACTAGTAAAGATTCATGTTAAAAA
 TTGGAGTACTAAGACGTGTCGATATATGATCATTTCTAAGTACAATTTTT
 N L M I L H S Y I L V K I H V K N>
 _____TRANSLATION OF 9E1_PEGFPCONSTRUCT (A)_____>

1710 1720 1730 1740 1750
 TGGAGATCACATGAAGGGGCTCGCATGCTCATTCGGGTGGCCAACAACA
 ACCTCTAGTGTACTTTCCCGAGCGTACGAGTAAGCCCCACCGTTGTTGT
 G D H M K G A R M L I R V A N N>
 _____TRANSLATION OF 9E1_PEGFPCONSTRUCT (A)_____>

1760 1770 1780 1790 1800
 TCAGCAATTTCCATCACACATTGTACCCATCCTGACGTCAACTGTGATT
 AGTCGTTTAAAGGTAGTGTCTAACATGGGTAGGACTGCAGTTGACACTPA
 I S K F P S H I V P I L T S T V I>
 _____TRANSLATION OF 9E1_PEGFPCONSTRUCT (A)_____>

1810 1820 1830 1840 1850
 GAGTGTACAGGGCAGGCCTGAAGAAGTCTGCTTTTCAGCTTCGCAGCTAT
 CTCACAGTGTCCCGTCCGGACTTCTTGAGACGAAAGTCGAAGCGTCGATA
 E C H R A G L K N S A F S F A A M>
 _____TRANSLATION OF 9E1_PEGFPCONSTRUCT (A)_____>

1860 1870 1880 1890 1900
 GTTGATGAGGCCTGAATACCGCAGCAAAATAGATGCCAAATACAAAAGA
 CAACTACTCCGGACTTATGGCGTCGTTTTATCTACGGTTTATGTTTTTCT
 L M R P E Y R S K I D A K Y K K>
 _____TRANSLATION OF 9E1_PEGFPCONSTRUCT (A)_____>

9E1_PEGFPconstruct Translated Sequence

1910 1920 1930 1940 1950
 AGATCGAGGGAATGGTCAGGAGACCCGATATATCTGAGATAGAAGAGGCC
 TCTAGCTCCCTTACCAGTCCTCTGGGCTATATAGACTCTATCTTCTCCGG
 K I E G M V R R P D I S E I E E A>
 _____TRANSLATION OF 9E1_PEGFPCONSTRUCT [A]_____>

1960 1970 1980 1990 2000
 ACGACTCCATGTCCATTCTGCAAATTTCTTCTCCCAGAGTGTGAACTCCT
 TGCTGAGGTACAGGTAAGACGTTTAAAGAAGAGGGTCTCACACTTGAGGA
 T T P C P F C K F L L P E C E L L>
 _____TRANSLATION OF 9E1_PEGFPCONSTRUCT [A]_____>

2010 2020 2030 2040 2050
 CTGTCCTGGATGTAAAAACAGTATCCCATATTGCATTGCAACAGGTGCGAC
 GACAGGACCTACATTTTTTGTGCATAGGGTATAACGTAACGTTGTCCAGCTG
 C P G C K N S I P Y C I A T G R>
 _____TRANSLATION OF 9E1_PEGFPCONSTRUCT [A]_____>

2060 2070 2080 2090 2100
 ACATGTTGAAAGATGACTGGACGGTGTGTCCACATTGTGACTTCCCTGCT
 TGTACAACCTTTCTACTGACCTGCCACACAGGTGTAACACTGAAGGGACGA
 H M L K D D W T V C P H C D F P A>
 _____TRANSLATION OF 9E1_PEGFPCONSTRUCT [A]_____>

2110 2120 2130 2140 2150
 CTATACTCAGAATTGAAGATCATGCTAAACACTGAAAGCACATGTCCTAT
 GATATGAGTCTTAACCTTCTAGTACGATTTGTGACTTTCGTGTACAGGATA
 L Y S E L K I M L N T E S T C P M>
 _____TRANSLATION OF 9E1_PEGFPCONSTRUCT [A]_____>

2160 2170 2180 2190 2200
 GTGTTTCAGAAAGATTAAACGCTGCTCAGCTGAAAAGATTTCAGACTGTA
 CACAAGTCTTTCTAATTTGCGACGAGTCGACTTTTCTAAAGTCTGACAT
 C S E R L N A A Q L K K I S D C>
 _____TRANSLATION OF 9E1_PEGFPCONSTRUCT [A]_____>

2210 2220 2230 2240 2250
 CCCAGTACCTGCGAACGGAGGAGGAACCTGGATCCACCGGTGCGCCACCATG
 GGGTCATGGACGCTTGCCCTCCTTGCACCTAGGTGGCCAGCGGTGGTAC
 T Q Y L R T E E E L D P P V A T M>
 _____TRANSLATION OF 9E1_PEGFPCONSTRUCT [A]_____>

2260 2270 2280 2290 2300
 GTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGGCCATCCTGGTCTGA
 CACTCGTTCCCGCTCCTCGACAAGTGGCCCCACCACGGGTAGGACCAGCT
 V S K G E E L F T G V V P I L V E>
 _____TRANSLATION OF 9E1_PEGFPCONSTRUCT [A]_____>

2310 2320 2330 2340 2350
 GCTGGACGGCGACGCTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCG
 CGACCTGCCGCTGCATTTGCCGGGTGTCAAGTCGCACAGGCCGCTCCCGC
 L D G D V N G H K F S V S G E G>
 _____TRANSLATION OF 9E1_PEGFPCONSTRUCT [A]_____>

2360 2370 2380 2390 2400
 AGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACC

9E1_pEGFPconstruct Translated Sequence

TCCCGCTACGGTGGATGCCGTTGCGACTGGGACTTCAAGTAGACGTGGTGG
E G D A T Y G K L T L K F I C T T>
____TRANSLATION OF 9E1_PEGFPCONSTRUCT (A)____>

2410 2420 2430 2440 2450
GGCAAGCTGCCCCGTGCCCTGGCCCCACCCTCGTGACCAACCTGACCTACGG
CCGTTTCGACGGGCACGGGACCGGGTGGGAGCACTGGTGGGACTGGATGCC
G K L P V P W P T L V T T L T Y G>
____TRANSLATION OF 9E1_PEGFPCONSTRUCT (A)____>

2460 2470 2480
CGTGCAAGTGCTTCAGCCGCTACCCCGACCAC
GCACGTCACGAAGTCGGCGATGGGGCTGGTG
V Q C F S R Y P D H>
____TRANSLATION OF 9E1_PEGFP____>